

# 2



PCT

## RAW SEQUENCE LISTING

DATE: 07/15/2004

PATENT APPLICATION: US/10/500,911

TIME: 10:18:10

Input Set : A:\3011 USOP seq.txt

Output Set: N:\CRF4\07152004\J500911.raw

3 <110> APPLICANT: NODA, Masakuni  
 4 MATSUO, Takanori  
 5 TSUGE, Hiroko  
 7 <120> TITLE OF INVENTION: Screening Method  
 9 <130> FILE REFERENCE: 3011 USOP  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/500,911  
 C--> 11 <141> CURRENT FILING DATE: 2004-07-08  
 11 <150> PRIOR APPLICATION NUMBER: PCT/JP03/00111  
 12 <151> PRIOR FILING DATE: 2003-01-01  
 14 <150> PRIOR APPLICATION NUMBER: JP 2002-3769  
 15 <151> PRIOR FILING DATE: 2002-01-10  
 17 <160> NUMBER OF SEQ ID NOS: 11  
 19 <170> SOFTWARE: PatentIn version 3.1  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 123  
 23 <212> TYPE: PRT  
 24 <213> ORGANISM: Homo sapiens  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: MISC FEATURE  
 28 <222> LOCATION: (1)..(123)  
 29 <223> OTHER INFORMATION: Partial amino acid sequence of Egr-1 protein which is  
 conserved  
 30 between human, mouse and rat.  
 32 <400> SEQUENCE: 1  
 33 Tyr Gln Ser Gln Leu Ile Lys Pro Ser Arg Met Arg Lys Tyr Pro Asn  
 34 1 5 10 15  
 35 Arg Pro Ser Lys Thr Pro Pro His Glu Arg Pro Tyr Ala Cys Pro Val  
 36 20 25 30  
 37 Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Glu Leu Thr Arg His  
 38 35 40 45  
 39 Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met  
 40 50 55 60  
 41 Arg Asn Phe Ser Arg Ser Asp His Leu Thr Thr His Ile Arg Thr His  
 42 65 70 75 80  
 43 Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala  
 44 85 90 95  
 45 Arg Ser Asp Glu Arg Lys Arg His Thr Lys Ile His Leu Arg Gln Lys  
 46 100 105 110  
 47 Asp Lys Lys Ala Asp Lys Ser Val Val Ala Ser  
 48 115 120  
 50 <210> SEQ ID NO: 2  
 51 <211> LENGTH: 543  
 52 <212> TYPE: PRT  
 53 <213> ORGANISM: Homo sapiens

ENTERED

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55 &lt;400&gt; SEQUENCE: 2

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56 Met Ala Ala Ala Lys Ala Glu Met Gln Leu Met Ser Pro Leu Gln Ile
57 1          5          10          15
58 Ser Asp Pro Phe Gly Ser Phe Pro His Ser Pro Thr Met Asp Asn Tyr
59          20          25          30
60 Pro Lys Leu Glu Glu Met Met Leu Leu Ser Asn Gly Ala Pro Gln Phe
61          35          40          45
62 Leu Gly Ala Ala Gly Ala Pro Glu Gly Ser Gly Ser Asn Ser Ser Ser
63          50          55          60
64 Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly Ser Asn Ser Ser
65 65          70          75          80
66 Ser Ser Ser Ser Thr Phe Asn Pro Gln Ala Asp Thr Gly Glu Gln Pro
67          85          90          95
68 Tyr Glu His Leu Thr Ala Glu Ser Phe Pro Asp Ile Ser Leu Asn Asn
69          100         105         110
70 Glu Lys Val Leu Val Glu Thr Ser Tyr Pro Ser Gln Thr Thr Arg Leu
71          115         120         125
72 Pro Pro Ile Thr Tyr Thr Gly Arg Phe Ser Leu Glu Pro Ala Pro Asn
73          130         135         140
74 Ser Gly Asn Thr Leu Trp Pro Glu Pro Leu Phe Ser Leu Val Ser Gly
75 145         150         155         160
76 Leu Val Ser Met Thr Asn Pro Pro Ala Ser Ser Ser Ser Ala Pro Ser
77          165         170         175
78 Pro Ala Ala Ser Ser Ala Ser Ala Ser Gln Ser Pro Pro Leu Ser Cys
79          180         185         190
80 Ala Val Pro Ser Asn Asp Ser Ser Pro Ile Tyr Ser Ala Ala Pro Thr
81          195         200         205
82 Phe Pro Thr Pro Asn Thr Asp Ile Phe Pro Glu Pro Gln Ser Gln Ala
83          210         215         220
84 Phe Pro Gly Ser Ala Gly Thr Ala Leu Gln Tyr Pro Pro Pro Ala Tyr
85 225         230         235         240
86 Pro Ala Ala Lys Gly Gly Phe Gln Val Pro Met Ile Pro Asp Tyr Leu
87          245         250         255
88 Phe Pro Gln Gln Gln Gly Asp Leu Gly Leu Gly Thr Pro Asp Gln Lys
89          260         265         270
90 Pro Phe Gln Gly Leu Glu Ser Arg Thr Gln Gln Pro Ser Leu Thr Pro
91          275         280         285
92 Leu Ser Thr Ile Lys Ala Phe Ala Thr Gln Ser Gly Ser Gln Asp Leu
93          290         295         300
94 Lys Ala Leu Asn Thr Ser Tyr Gln Ser Gln Leu Ile Lys Pro Ser Arg
95 305         310         315         320
96 Met Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Pro His Glu Arg
97          325         330         335
98 Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser
99          340         345         350
100 Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys Pro Phe
101          355         360         365
102 Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu Thr
103          370         375         380

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104 Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile
105 385                      390                      395                      400
106 Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys Arg His Thr Lys
107                      405                      410                      415
108 Ile His Leu Arg Gln Lys Asp Lys Lys Ala Asp Lys Ser Val Val Ala
109                      420                      425                      430
110 Ser Ser Ala Thr Ser Ser Leu Ser Ser Tyr Pro Ser Pro Val Ala Thr
111                      435                      440                      445
112 Ser Tyr Pro Ser Pro Val Thr Thr Ser Tyr Pro Ser Pro Ala Thr Thr
113                      450                      455                      460
114 Ser Tyr Pro Ser Pro Val Pro Thr Ser Phe Ser Ser Pro Gly Ser Ser
115 465                      470                      475                      480
116 Thr Tyr Pro Ser Pro Val His Ser Gly Phe Pro Ser Pro Ser Val Ala
117                      485                      490                      495
118 Thr Thr Tyr Ser Ser Val Pro Pro Ala Phe Pro Ala Gln Val Ser Ser
119                      500                      505                      510
120 Phe Pro Ser Ser Ala Val Thr Asn Ser Phe Ser Ala Ser Thr Gly Leu
121                      515                      520                      525
122 Ser Asp Met Thr Ala Thr Phe Ser Pro Arg Thr Ile Glu Ile Cys
123                      530                      535                      540

```

125 &lt;210&gt; SEQ ID NO: 3

126 &lt;211&gt; LENGTH: 1629

127 &lt;212&gt; TYPE: DNA

128 &lt;213&gt; ORGANISM: Homo sapiens

130 &lt;220&gt; FEATURE:

131 &lt;221&gt; NAME/KEY: CDS

132 &lt;222&gt; LOCATION: (1)..(1629)

133 &lt;223&gt; OTHER INFORMATION:

W--&gt; 135 &lt;400&gt; 3

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136 atg gcc gcg gcc aag gcc gag atg cag ctg atg tcc ccg ctg cag atc      48
137 Met Ala Ala Ala Lys Ala Glu Met Gln Leu Met Ser Pro Leu Gln Ile
138 1                      5                      10                      15
139 tct gac ccg ttc gga tcc ttt cct cac tcg ccc acc atg gac aac tac      96
140 Ser Asp Pro Phe Gly Ser Phe Pro His Ser Pro Thr Met Asp Asn Tyr
141                      20                      25                      30
142 cct aag ctg gag gag atg atg ctg ctg agc aac ggg gct ccc cag ttc      144
143 Pro Lys Leu Glu Glu Met Met Leu Leu Ser Asn Gly Ala Pro Gln Phe
144                      35                      40                      45
145 ctc ggc gcc gcc ggg gcc cca gag ggc agc ggc agc aac agc agc agc      192
146 Leu Gly Ala Ala Gly Ala Pro Glu Gly Ser Gly Ser Asn Ser Ser Ser
147                      50                      55                      60
148 agc agc agc ggg ggc ggt gga ggc ggc ggg ggc ggc agc aac agc agc      240
149 Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Ser Asn Ser Ser
150 65                      70                      75                      80
151 agc agc agc agc acc ttc aac cct cag gcg gac acg ggc gag cag ccc      288
152 Ser Ser Ser Ser Thr Phe Asn Pro Gln Ala Asp Thr Gly Glu Gln Pro
153                      85                      90                      95
154 tac gag cac ctg acc gca gag tct ttt cct gac atc tct ctg aac aac      336
155 Tyr Glu His Leu Thr Ala Glu Ser Phe Pro Asp Ile Ser Leu Asn Asn

```

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156	100	105	110	
157	gag aag gtg ctg gtg gag acc agt tac ccc agc caa acc act cga ctg	384		
158	Glu Lys Val Leu Val Glu Thr Ser Tyr Pro Ser Gln Thr Thr Arg Leu			
159	115 120 125			
160	ccc ccc atc acc tat act ggc cgc ttt tcc ctg gag cct gca ccc aac	432		
161	Pro Pro Ile Thr Tyr Thr Gly Arg Phe Ser Leu Glu Pro Ala Pro Asn			
162	130 135 140			
163	agt ggc aac acc ttg tgg ccc gag ccc ctc ttc agc ttg gtc agt ggc	480		
164	Ser Gly Asn Thr Leu Trp Pro Glu Pro Leu Phe Ser Leu Val Ser Gly			
165	145 150 155 160			
166	cta gtg agc atg acc aac cca ccg gcc tcc tcg tcc tca gca cca tct	528		
167	Leu Val Ser Met Thr Asn Pro Pro Ala Ser Ser Ser Ser Ala Pro Ser			
168	165 170 175			
169	cca gcg gcc tcc tcc gcc tcc gcc tcc cag agc cca ccc ctg agc tgc	576		
170	Pro Ala Ala Ser Ser Ala Ser Ala Ser Gln Ser Pro Pro Leu Ser Cys			
171	180 185 190			
172	gca gtg cca tcc aac gac agc agt ccc att tac tca gcg gca ccc acc	624		
173	Ala Val Pro Ser Asn Asp Ser Ser Pro Ile Tyr Ser Ala Ala Pro Thr			
174	195 200 205			
175	ttc ccc acg ccg aac act gac att ttc cct gag cca caa agc cag gcc	672		
176	Phe Pro Thr Pro Asn Thr Asp Ile Phe Pro Glu Pro Gln Ser Gln Ala			
177	210 215 220			
178	ttc ccg gcc tcg gca ggg aca gcg ctc cag tac ccg cct cct gcc tac	720		
179	Phe Pro Gly Ser Ala Gly Thr Ala Leu Gln Tyr Pro Pro Pro Ala Tyr			
180	225 230 235 240			
181	cct gcc gcc aag ggt ggc ttc cag gtt ccc atg atc ccc gac tac ctg	768		
182	Pro Ala Ala Lys Gly Gly Phe Gln Val Pro Met Ile Pro Asp Tyr Leu			
183	245 250 255			
184	ttt cca cag cag cag ggg gat ctg ggc ctg ggc acc cca gac cag aag	816		
185	Phe Pro Gln Gln Gln Gly Asp Leu Gly Leu Gly Thr Pro Asp Gln Lys			
186	260 265 270			
187	ccc ttc cag ggc ctg gag agc cgc acc cag cag cct tcg cta acc cct	864		
188	Pro Phe Gln Gly Leu Glu Ser Arg Thr Gln Gln Pro Ser Leu Thr Pro			
189	275 280 285			
190	ctg tct act att aag gcc ttt gcc act cag tcg ggc tcc cag gac ctg	912		
191	Leu Ser Thr Ile Lys Ala Phe Ala Thr Gln Ser Gly Ser Gln Asp Leu			
192	290 295 300			
193	aag gcc ctc aat acc agc tac cag tcc cag ctc atc aaa ccc agc cgc	960		
194	Lys Ala Leu Asn Thr Ser Tyr Gln Ser Gln Leu Ile Lys Pro Ser Arg			
195	305 310 315 320			
196	atg cgc aag tat ccc aac cgg ccc agc aag acg ccc ccc cac gaa cgc	1008		
197	Met Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Pro His Glu Arg			
198	325 330 335			
199	cct tac gct tgc cca gtg gag tcc tgt gat cgc cgc ttc tcc cgc tcc	1056		
200	Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser			
201	340 345 350			
202	gac gag ctc acc cgc cac atc cgc atc cac aca ggc cag aag ccc ttc	1104		
203	Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys Pro Phe			
204	355 360 365			

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Output Set: N:\CRF4\07152004\J500911.raw

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205 cag tgc cgc atc tgc atg cgc aac ttc agc cgc agc gac cac ctc acc      1152
206 Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu Thr
207      370                      375                      380
208 acc cac atc cgc acc cac aca ggc gaa aag ccc ttc gcc tgc gac atc      1200
209 Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile
210 385                      390                      395                      400
211 tgt gga aga aag ttt gcc agg agc gat gaa cgc aag agg cat acc aag      1248
212 Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys Arg His Thr Lys
213                      405                      410                      415
214 atc cac ttg cgg cag aag gac aag aaa gca gac aaa agt gtt gtg gcc      1296
215 Ile His Leu Arg Gln Lys Asp Lys Lys Ala Asp Lys Ser Val Val Ala
216                      420                      425                      430
217 tct tcg gcc acc tcc tct ctc tct tcc tac ccg tcc ccg gtt gct acc      1344
218 Ser Ser Ala Thr Ser Ser Leu Ser Ser Tyr Pro Ser Pro Val Ala Thr
219      435                      440                      445
220 tct tac ccg tcc ccg gtt act acc tct tat cca tcc ccg gcc acc acc      1392
221 Ser Tyr Pro Ser Pro Val Thr Ser Tyr Pro Ser Pro Ala Thr Thr
222      450                      455                      460
223 tca tac cca tcc cct gtg ccc acc tcc ttc tcc tct ccc ggc tcc tcg      1440
224 Ser Tyr Pro Ser Pro Val Pro Thr Ser Phe Ser Ser Pro Gly Ser Ser
225 465                      470                      475                      480
226 acc tac cca tcc cct gtg cac agt ggc ttc ccc tcc ccg tcg gtg gcc      1488
227 Thr Tyr Pro Ser Pro Val His Ser Gly Phe Pro Ser Pro Ser Val Ala
228                      485                      490                      495
229 acc acg tac tcc tct gtt ccc cct gct ttc ccg gcc cag gtc agc agc      1536
230 Thr Thr Tyr Ser Ser Val Pro Pro Ala Phe Pro Ala Gln Val Ser Ser
231                      500                      505                      510
232 ttc cct tcc tca gct gtc acc aac tcc ttc agc gcc tcc aca ggg ctt      1584
233 Phe Pro Ser Ser Ala Val Thr Asn Ser Phe Ser Ala Ser Thr Gly Leu
234      515                      520                      525
235 tcg gac atg aca gca acc ttt tct ccc agg aca att gaa att tgc      1629
236 Ser Asp Met Thr Ala Thr Phe Ser Pro Arg Thr Ile Glu Ile Cys
237      530                      535                      540

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239 <210> SEQ ID NO: 4
240 <211> LENGTH: 1629
241 <212> TYPE: DNA
242 <213> ORGANISM: Homo sapiens
244 <220> FEATURE:
245 <221> NAME/KEY: CDS
246 <222> LOCATION: (1)..(1629)
247 <223> OTHER INFORMATION:

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W--&gt; 249 &lt;400&gt; 4

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250 atg gcc gcg gcc aag gcc gag atg cag ctg atg tcc ccg ctg cag atc      48
251 Met Ala Ala Ala Lys Ala Glu Met Gln Leu Met Ser Pro Leu Gln Ile
252 1                      5                      10                      15
253 tct gac ccg ttc gga tcc ttt cct cac tcg ccc acc atg gac aac tac      96
254 Ser Asp Pro Phe Gly Ser Phe Pro His Ser Pro Thr Met Asp Asn Tyr
255      20                      25                      30
256 cct aag ctg gag gag atg atg ctg ctg agc aac ggg gct ccc cag ttc      144

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/500,911

DATE: 07/15/2004  
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Input Set : A:\3011 USOP seq.txt  
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11

**VERIFICATION SUMMARY**

PATENT APPLICATION: **US/10/500,911**

DATE: 07/15/2004

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Input Set : **A:\3011 USOP seq.txt**

Output Set: **N:\CRF4\07152004\J500911.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application No  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:135 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:133  
L:249 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:247